IN THE SPECIFICATION

Please replace the paragraph beginning on page 10, line 25 with the following amended paragraph:

The primers herein are selected to be "substantially" complementary to the different strands of each specific sequence to be amplified. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and thereby form a template for synthesis of the extension product of the other primer. Computer generated searches using programs such as Primer3 ~~(www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi)~~ (available on the worldwide web at genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline ~~(www-genome.wi.mit.edu/cgi-bin/www-STS-Pipeline)~~ (available on the worldwide web at genome.wi.mit.edu/cgi-bin/www-STS Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques* *25*:112-123 (1998)), for example, can be used to identify potential PCR primers. Exemplary primers include primers that are 18 to 50 bases long, where at least between 18 to 25 bases are identical or complementary to at least 18 to 25 bases segment of the template sequence.

Please replace the paragraph beginning on page 38, line 9, with the following amended paragraph:

Real time detection of RT-PCR is carried out using the ABI®7700 Sequence detection system from PE Applied Biosytems following the protocols found on ~~http://www.pebio.com~~ the worldwide web at pebio.com. The amount of the 3'untranslated region is determined by relative quantitation. The 18S rRNA endogenous control is used to normalize the expression of the 3' untranslated region. The availability of distinguishable reporter dyes for the ABI®7700 Sequence detection system makes it possible to amplify and detect the target amplicon and the endogenous control amplicon in the same tube (*i.e.*, multiplex PCR). A calibrator transgenic line is chosen preferably to compare individual experimental Δ Ct values to generate $\Delta\Delta$Ct values. A calibrator transgenic line is one whose expression has been relatively quantitated using a different method such as Northern Blotting. The relative gene expression between the calibrator line and the experimental line containing the untranslated 3' end of the *Pisum sativum* rbcS E9 gene is calculated as $2^{-\Delta\Delta Ct}$.

Please replace the paragraph beginning on page 37, line 16, with the following amended paragraph:

Three hole punches of leaves from *Arabidopsis thaliana* are flash frozen in liquid nitrogen. The frozen tissue is subsequently freeze dried for a period of 48 hours. The freeze dried tissue is placed in a 1.4 ml tube with a glass bead (3 mm), capped ;and

pulverized into a fine powder using a Retsch model MM300 laboratory vibration mill. RNA is extracted according to the Qiagen ™ (Valencia, CA) Rneasy Plant Mini kits (Catalogue number 74904). RT-PCR reactions and thermocycling conditions are according to the Taqman™ One Step RT-PCR Master Mix Reagents Kit (Perkin Elmer Applied Biosystems, Foster City, CA). Approximately 40 ng of total RNA is used per reaction with a final concentration of 300 nM of primer pair targeting SEQ ID NO: [[3]] 2, the 3' untranslated region of the *Pisum sativum* rbcS E9 gene. This 3' untranslated region is used as the second nucleic acid molecule to detect the expression of a first transgenic nucleic acid molecule which may be any gene operably linked and co-expressed with it. The primers targeting this 3' untranslated region are listed in SEQ ID NO: 7, SEQ ID NO: 8 and SEQ ID NO: 28. SEQ ID NO: 7 may be used with either SEQ ID NO: 8 or SEQ ID NO: 28. A final concentration of 200 nM of probe (SEQ ID NO: 9) is used along with a final concentration of 20 nM of 18S rRNA endogenous control primer and a final concentration of 50 nM endogenous 18S rRNA control probe. The probes are labeled at the 5' end with FAM and on the 3' end with TAMRA. Primers and probes are selected with Primer Express software Version 1.0 (PE Applied Biosystems) using default values.